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Commensurability and cross-study inference in quantitative species interaction networks

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Abstract

Macroecological inference increasingly seeks to characterize community topology using species interaction networks. Since collecting new networks at a global scale is rarely feasible, researchers instead reuse open-access networks sourced from independent publications. While this immediately enables comparison across broad spatial scales, analyses that aim to infer general rules of network topology require treating these networks as commensurable despite substantial heterogeneity in the drivers of topology, including differences in (1) sampling design (e.g., temporal and spatial scale), (2) network construction (e.g., link definition), and (3) biological and environmental factors. Here, we operationalize this three-class framework and apply it to a collection of open-access quantitative bipartite networks. Using this approach, we show that drivers of topology within all three classes are overwhelmingly publication-specific. When we quantify topology directly, common methods intended to improve commensurability do not remove this publication-specific structure: sampling intensity tracks network size, which can itself reflect sampling extent, and topological similarity within publications persists after both null model correction and rarefaction to a standardized number of interactions. Accounting for publication identity offers only a partial remedy, since many publications contribute only a single network, leaving no within-publication replication with which to separate publication-specific effects from those unique to that network. We therefore argue that realizing the full promise of network macroecology requires prioritizing comparability through standardized and network coordinated data collection and reporting. We discuss the implications of adopting these changes for future network syntheses.

KEYWORDS
bipartite networks, data comparability, methodological heterogeneity, network null models, network size, open-access data, rarefaction, sampling heterogeneity, sampling intensity

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INTRODUCTION

Since its emergence in the 1970s, quantitative network ecology has matured into a field with a substantial body of theory supporting analyses of how biotic and abiotic conditions, species traits, and evolutionary history shape communities (Delmas et al., 2019; Dormann et al., 2009, 2017; Dunne, 2006; Gauzens et al., 2025; Pringle & Hutchinson, 2020). In these networks, nodes typically correspond to species and links encode their interactions, giving rise to their alternative name *species interaction networks* (e.g., Berryman, 1993; Higashi & Nakajima, 1995), also commonly simplified to *networks*. Beyond their use in fundamental ecological research, species interaction networks have attracted conservation-oriented researchers. Here, they are promoted as tools for broadening preservation efforts beyond individual species by additionally making explicit the interactions that practitioners must consider to ensure species persistence (Harvey et al., 2017; Tylianakis et al., 2010).

Given the tremendous resources needed to sample communities to build novel networks, researchers—including ourselves—are regularly constrained to reuse open-access species interaction networks in our own work (e.g., Brimacombe, Bodner, Michalska-Smith, et al., 2022; Cirtwill et al., 2015; García-Callejas et al., 2026). These networks, of which there are hundreds, are typically sourced from different published primary articles and made available either directly through open-data repositories associated with individual studies or through centralized network repositories (Figure 1). Examples of the latter include *Interaction Web DataBase* (http://www.ecologia.ib.usp.br/iwdb/), *Web-of-life* (`web-of-life.es`: Fortuna et al., 2014), R package *EuPPollNet* (Lanuza et al., 2025), *Mangal* (https://mangal.io: Poisot et al., 2016), and the compilation by Fricke and Svenning (2020). The ease with which species interaction networks can be obtained from these sources has likely contributed to their greater reuse (Xing & Fayle, 2021).

The repeated reuse of any ecological data, including open-access networks, however, is an increasingly recognized epistemological issue (Devictor & Bensaude-Vincent, 2016; Foster et al., 2021; Lindenmayer & Likens, 2013). When the same datasets are analyzed to search for general patterns, it becomes essential to distinguish exploratory synthesis from confirmatory inference (Ford, 2000). Exploratory

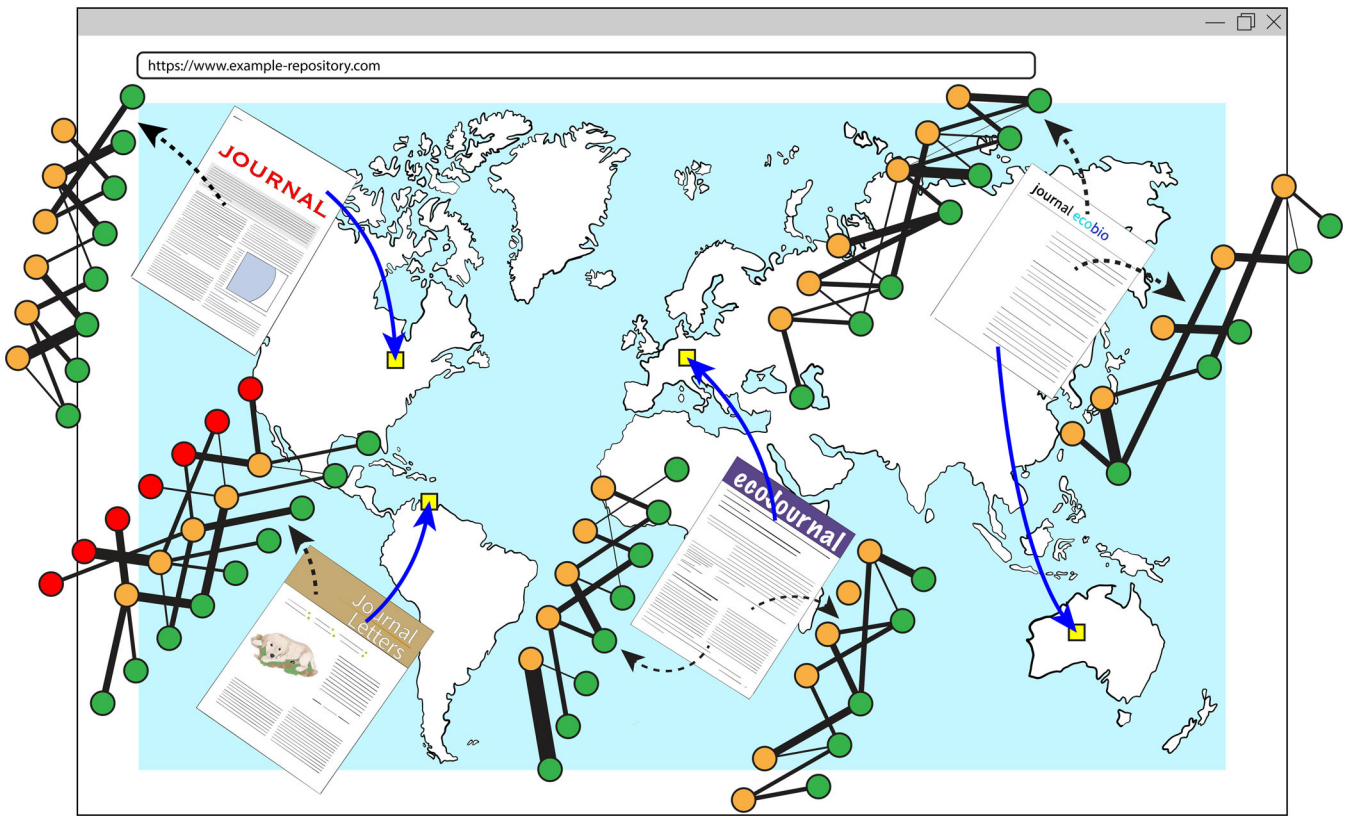

FIGURE 1 Example of a quantitative open-access species interaction network centralized repository (e.g., Fortuna et al., 2014; Fricke & Svenning, 2020; Lanuza et al., 2025; Poisot et al., 2016) collated from source publications (dashed arrows), whose networks were sampled and constructed to represent communities at different locations (blue arrows to yellow squares). Publications can either produce a single network or multiple networks. Illustration by Chris Brimacombe.

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analyses are indeed valuable for generating hypotheses, but testing generated hypotheses ultimately requires evaluation using new data (Burnham & Anderson, 2002). For the many studies that rely on large sets of open-access networks, this means that their hypotheses are exceedingly difficult to test directly since collecting novel network data at comparable scales is prohibitively costly.

Nevertheless, comparing open-access species interaction networks is also difficult from a network methodological basis. Since both data collection and network construction are tailored to the specific aims and context of the original study (Closs & Lake, 1994; Gauzens et al., 2025; Mestre et al., 2022), they may not represent comparable measurements of a common ecological community property. Instead, open-access networks may represent different observational constructs expressed in a common network form (Brimacombe et al., 2025). Pooled analyses thus require treating open-access networks as commensurable, despite their many differences. Such commensurability is typically presumed when methods intended to improve comparability (e.g., rarefaction, null model corrections) are applied in statistical analyses (Blüthgen & Staab, 2024), although the effectiveness of these methods is rarely assessed in the context of cross-study network pooling.

Within this broader problem of commensurability, the reuse of open-access networks involves balancing the number of networks available for analysis against the information retained about interaction strength. This trade-off is inherent in the choice between binary networks, in which links between nodes indicate only whether an interaction occurred between two species, and quantitative networks, in which weighted edges additionally capture its magnitude (e.g., the number of flower visits by a hummingbird; Arizmendi & Ornelas, 1990). When conducting pooled open-access network analyses, opting to reuse binary networks substantially expands the set of networks available for cross-study analysis. This greater availability likely arises for two reasons. First, estimating interaction strengths requires additional sampling effort (Banville et al., 2025; Strydom et al., 2021), which may discourage researchers from constructing quantitative networks in the first place. Second, quantitative networks can always be reduced to binary networks (e.g., Brimacombe, Bodner, Michalska-Smith, et al., 2022), allowing them to be pooled alongside networks originally constructed as binary. At the same time, quantitative networks have been argued to be more robust to sampling variation and provide greater biological insight, reflecting real interaction strengths between species (Banašek-Richter et al., 2004; Blüthgen, 2010; Fründ et al., 2016; Henriksen et al., 2019; Nielsen & Bascompte, 2007; Pinheiro et al., 2022; Vizentin-Bugoni et al., 2016). It remains largely untested, however, whether this proposed benefit of quantitative networks can mitigate these larger sampling differences when networks are pooled across diverse publications.

In this *Concepts and Synthesis*, we build on our conceptual framework developed in Brimacombe et al. (2023, 2025), which organizes drivers of network topology into three broad classes encompassing *sampling strategies*, *network construction methodologies*, and *biological and environmental factors*, to examine how comparability issues arise among quantitative open-access bipartite networks sourced from different studies. Specifically, we evaluate whether *sampling*- and *construction*-related drivers of topological variation are likely to remain evident even in this information-rich quantitative network dataset. We then test whether several widely used methods mitigate these issues and support meaningful cross-study comparison. We conclude by outlining practical next steps, including recommendations for designing a next generation of open-access networks and the implications for cross-study inference.

CASE STUDY OF OPEN-ACCESS QUANTITATIVE BIPARTITE NETWORKS

To illustrate our framework, we drew on quantitative bipartite networks from two online centralized repositories (archived with the data in Archived_networks_and_publication_sources.pdf). The networks available through these resources were themselves compiled from existing studies. *Web-of-life* assembled networks primarily from published studies, obtaining data from associated appendices or repositories or directly from authors, with some additional contributed datasets (Fortuna et al., 2014), whereas Fricke and Svenning (2020) assembled their seed-dispersal networks through an extensive literature search. Consequently, these compilations are not exhaustive and their contents depend partly on which networks were published, accessible, and identified for inclusion. However, since such compilations provide centralized and readily accessible collections of species interaction networks (Brimacombe et al., 2023), they are commonly reused for comparative analyses and therefore represent precisely the type of open-access data for which assessing cross-study comparability is important.

We applied several inclusion and curation criteria to networks obtained from these sources. Given the sensitivity of very small networks to sampling effects (Henriksen et al., 2019), we only included those with at least five animal and five plant nodes. This removed 5 pollination networks and 97 seed-dispersal networks. We also manually verified the taxonomic names of nodes and made 112 corrections (archived with the

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data in Archived_taxonomic_name_corrections.pdf). Since we later performed Patefield null model analyses on our networks (Dormann et al., 2008), we were restricted to those originally reported with integer edge weights.

The resulting dataset comprised 279 networks, of which 113 were pollination networks from *Web-of-life* (Fortuna et al., 2014) and 166 were seed-dispersal networks from Fricke and Svenning (2020). Of those, 122 were from publications that contributed a single network: 31 pollination networks from 31 publications and 91 seed-dispersal networks from 91 publications. The remaining 157 were drawn from 25 publications that each contributed multiple networks, comprising 82 pollination networks from seven publications and 75 seed-dispersal networks from 18 publications. These networks were geographically biased towards Central and South America and the (sub)tropics (Appendix S1: Figure S1), reflecting broader gaps in the available data, particularly from Asia (Cameron et al., 2019; Poisot et al., 2021).

All analyses were conducted in R version 4.6.1 (R Core Team, 2026). All analysis code and package information are available in the archived repository.

FRAMEWORK FOR CATEGORIZING DRIVERS OF NETWORK TOPOLOGY

Our expanded three-class framework organizes topological drivers according to the successive stages through which species interaction networks are generated (Table 1). Although we apply the framework here to quantitative bipartite networks, it is intended to describe drivers of topology across all types of species interaction networks (e.g., food webs, binary networks). First, the *sampling strategies* class consists of the topological drivers expressed in the structure of networks due to the decisions researchers make when observing species and their interactions in the field. For example, the amount of area sampled can influence network complexity (Galiana et al., 2022). The *network construction methodologies* class encompasses topological drivers that shape network structure through researchers' choices about how observations are encoded into the network (e.g., which organisms are included; Goldwasser & Roughgarden, 1993, the temporal extent represented by the network; CaraDonna et al., 2017; CaraDonna & Waser, 2020). Finally, *biological and environmental factors* comprise the biotic and abiotic drivers that shape which species and interactions occur in nature. These drivers are often the primary focus of ecological inference, for example, when evaluating how biogeographical gradients structure bipartite networks (García-Callejas et al., 2026; Schleuning et al., 2014; Song et al., 2017; Welti & Joern, 2015).

Applying this framework to one of Cruz et al. (2013)'s open-access bipartite networks illustrates how these classes of topological drivers can be expressed in practice (Figure 2). In this example network, *sampling strategies* largely reflect how researchers were only interested in collecting observations of seed-dispersing birds. To sample

TABLE 1 A framework for three classes of drivers of network topology.

Class	Driver	Description
Sampling strategies	Equipment and protocols	Sampling methods and field protocols used to detect species and interactions (e.g., camera traps, direct observation), including differences in detectability across taxa and interaction types
	Temporal and spatial design	The frequency and spatial grain of sampling within the study period (e.g., revisit interval), as well as the total duration and geographic area covered
	Targeting rules	Rules that define the focal taxa and interactions (e.g., restricting to birds or insects; focal plant sampling)
Network construction methodologies	Node resolution	Taxonomic resolution of nodes (e.g., species, genus) and decisions about retaining unresolved taxa
	Edge weights	Whether edges are weighted, and how weights are defined (e.g., counts, rates, presence–absence)
	Aggregation choice	How observations are pooled across time, space, or replicates (e.g., site-level vs. pooled networks; seasonal vs. annual networks)
Biological and environmental factors	Climate	Local climatic conditions that shape species activity, phenology, and interaction opportunities
	Habitat	Habitat type (e.g., vegetation structure, land-use intensity) that influences community composition and interaction opportunities
	Species traits	Traits that shape interaction feasibility and strength (e.g., body size, morphology, diet breadth, phenology)

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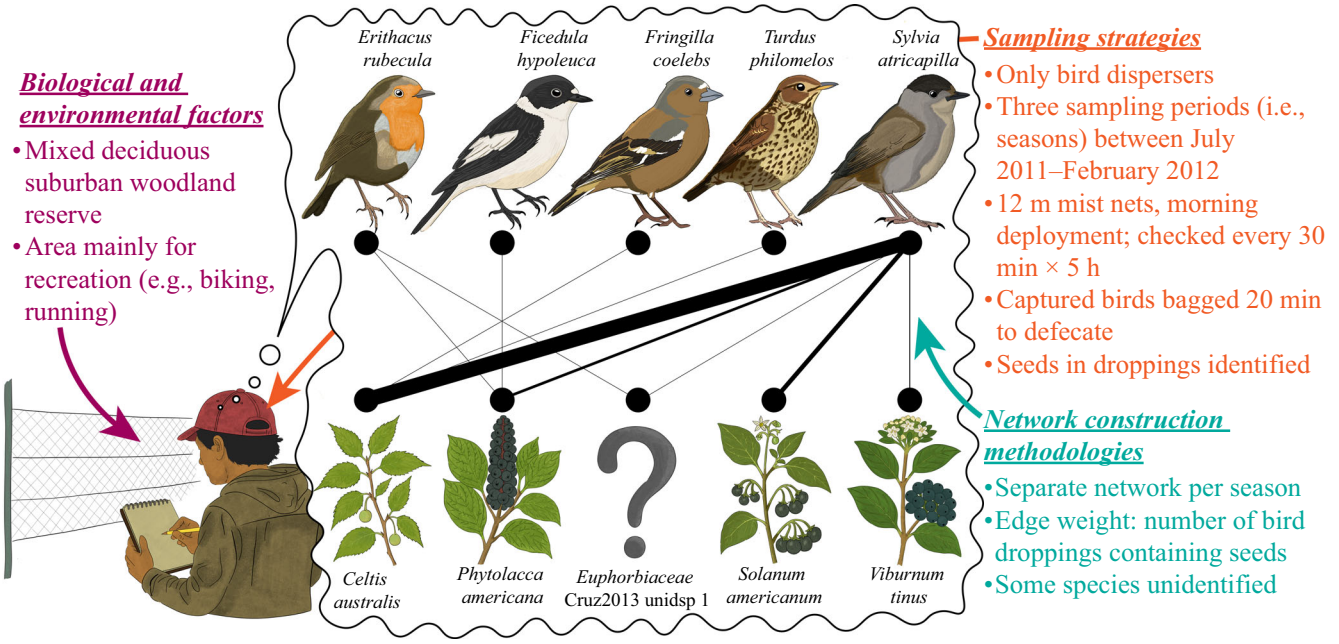

FIGURE 2 Illustration of how the three classes of topological drivers (i.e., *sampling strategies* [orange text], *network construction methodologies* [aqua text], and *biological and environmental factors* [purple text]) uniquely shape the quantitative autumn seed-dispersal network built by Cruz et al. (2013). Illustration by Chris Brimacombe.

the bird community, they used mist-nets across three seasons between July 2011 and February 2012, deployed for 5 h at a time. Entangled birds were then placed in a bag for 20 min to defecate, and the seeds present in their droppings were used to identify interactions between bird and plant species. These observations were subsequently shaped by several *network construction methodologies* including the construction of separate seasonal networks, weighting interactions by the number of bird droppings containing seeds of each plant species, and retaining some unidentified species as nodes (e.g., *Euphorbiaceae* unidsp 1). The *biological and environmental factors*, in turn, reflected the local context in which these interactions occurred, in this case a mixed deciduous woodland reserve in Portugal that was also mainly used for recreation.

THREE CLASSES OF TOPOLOGICAL DRIVERS AND THEIR PUBLICATION-SPECIFIC EXPRESSION ACROSS OPEN-ACCESS NETWORKS

While species interaction networks are typically built to address specific research questions (Closs & Lake, 1994; Gauzens et al., 2025; Mestre et al., 2022), it remains unknown to what extent these publication-specific decisions result in possible publication-specific topological drivers across open-access networks. Unfortunately, a complete accounting is intractable since many drivers are not reported in sufficient detail (e.g., Kita et al., 2022; Poisot et al., 2016). We find this to be especially true for drivers that are not directly encoded in the network's nodes and edges. The spatial extent (i.e., amount of area sampled) is one particularly salient illustration, where networks are described in vastly different ways or may be missing altogether. For example, Ollerton et al. (2003) describe their network as representing an 8-ha site, whereas Vizentin-Bugoni et al. (2016) built a single-site network by pooling observations collected along 12 km of trails. In some cases, key information can also be missing altogether such as Bezerra et al. (2009) that report that 138 individual plants were monitored without specifying the spatial extent over which they were sampled. The absence of standardized metadata that would make these differences explicit and quantifiable therefore makes it difficult to determine how commensurable open-access networks are.

Using the information available, we apply our framework in the next three subsections to characterize variation in selected topological drivers across the 279 open-access bipartite networks. The drivers in Table 1 represent the broad set of processes encompassed by each class, and the analyses below focus on those that could be characterized sufficiently consistently across the available networks and their source publications. This allows us to assess the extent to which differences in *sampling strategies*, *network construction methodologies*, and *biological*

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and environmental factors challenge treating these networks as commensurable.

Sampling strategies

Differences in species composition

Networks built from selective subsets of species can emphasize particular topological patterns. For instance, the trait of beak morphology can guide resource use in birds (Dalsgaard et al., 2021; Grant & Grant, 2007), and consequently choosing which birds to sample will influence the links and edge weights in networks. Similarly, interactions are shaped by behavioral traits (Aubert et al., 2026; Barreto et al., 2025; Maruyama et al., 2015) and phenology (Gonzalez & Loiselle, 2016; Peralta et al., 2020), while interaction patterns also exhibit phylogenetic signal (Peralta, 2016; Segar et al., 2020).

Such species selectivity can therefore introduce substantial compositional differences among networks drawn from different studies, with potential consequences for network topology (Mello & Dormann, 2025). To evaluate these differences while limiting the influence of publication-specific variation in taxonomic resolution, we restricted β-diversity calculations to nodes identified to species level. When β-diversity was calculated separately for animal and plant guilds within each interaction type, median within-publication β-diversity ranged from 0.50 to 0.77, whereas the between-publication median was 1.00 (Figure 3). Thus, species composition differed more markedly between publications than within them. Geographic distance also explained substantial variation in species composition, although its explanatory contribution strongly overlapped with that of publication identity, particularly for pollination networks (Appendix S1: Section S2). Consequently, these compositional differences cannot be attributed to publication-specific targeting alone, but neither can geographic separation account for all of the publication-associated structure observed across network types and guilds.

Publication-specific targeting nonetheless provides one mechanism through which studies can systematically differ in the species represented in their networks. Among the seven source publications that produced multiple pollination networks, some restricted their animal guild to hummingbirds (Dalsgaard et al., 2021; Graham & Weinstein, 2018; Maruyama et al., 2015; Partida-Lara et al., 2018), others to insects (Dicks et al., 2002), and only a few included arthropods and vertebrates (Kaiser-Bunbury et al., 2010, 2014). More broadly, studies may also differ in the types of interactions they choose to target, meaning that pollination, seed dispersal, or other interaction networks can represent different subsets of the interactions occurring within a broader ecological community (García-Callejas et al., 2018).

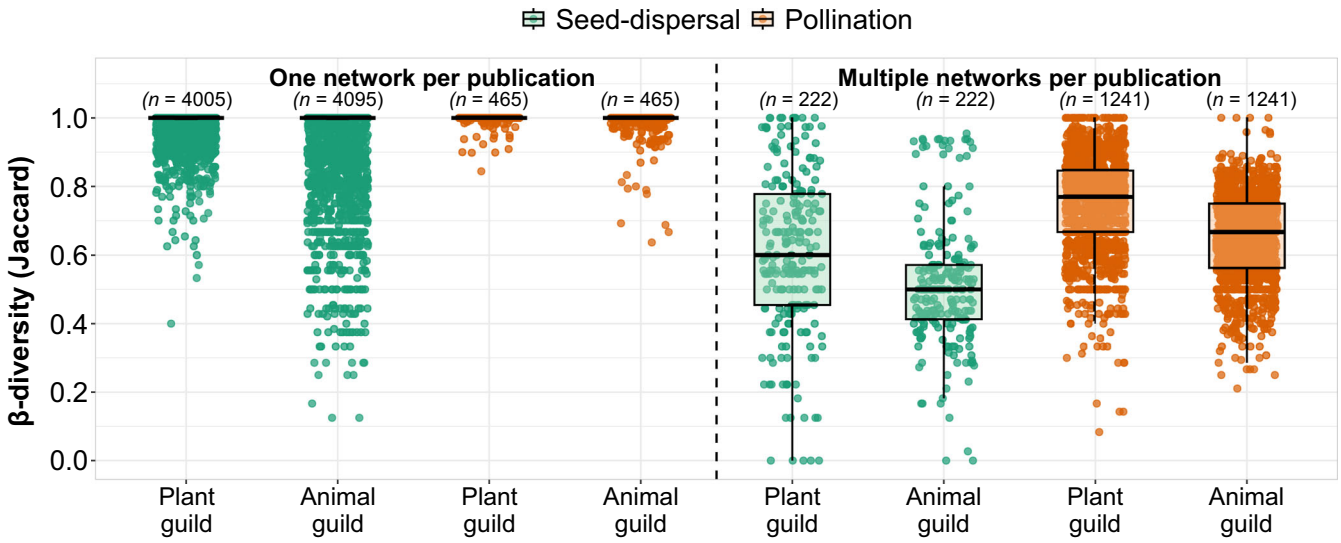

FIGURE 3 Pairwise β-diversity among 113 pollination and up to 166 seed-dispersal quantitative networks, calculated using only nodes identified to species level. All 113 pollination networks were retained for both guilds. For seed-dispersal networks, all 166 were retained for the animal guild and 165 for the plant guild, with one network excluded from the latter after no plant nodes identified to species level remained. Comparisons were restricted to within-guild pairs (animal or plant) and were calculated separately for (1) publications contributing a single network and (2) publications contributing multiple networks; in the latter case, comparisons were further restricted to networks from the same publication. Higher β-diversity indicates lower species compositional similarity. Labels indicate the number of pairwise comparisons; for n networks, this equals $n(n-1)/2$.

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Publication-specific targeting decisions therefore determine which taxa and interactions are represented before any differences in ecological processes are considered, providing a mechanism through which differences in sampling focus can contribute to publication-specific variation in network topology.

Differences in interaction-recording approaches

Open-access networks are sampled using diverse in situ field recording approaches (Dunne, 2006; Gibson et al., 2011; Jordano, 2016; Quintero et al., 2022; Vázquez et al., 2022; Vitorino et al., 2022), which differ in how interactions are observed and thus which interaction events enter the resulting network. These recording approaches reflect study goals (e.g., Devictor et al., 2010), and as study goals are wide-ranging, such diversity across open-access networks is the rule, rather than the exception.

In our open-access networks, variation in interaction-recording approaches is pervasive (top panel of Figure 4) and occurs primarily between studies. Publications that contributed multiple networks almost always used the same interaction-recording approach, or the same combination of approaches, across their networks (except Galetti & Pizo, 1996). To prevent publications contributing many networks from disproportionately influencing our results, we aggregated networks from the same publication when they shared an identical recording approach. Under this aggregation, pollination networks most often relied on observer-based approaches such as transect walks (32%), targeted fauna (13%), or flora surveys (11%), whereas seed-dispersal networks relied heavily on mist-netting (45%) and, to a lesser extent, focal plant observations (20%). Such differences can translate into measurable topological variation, even when attempts are made to statistically account for sampling focus (Sørensen et al., 2011). For instance, Gibson et al. (2011) showed that

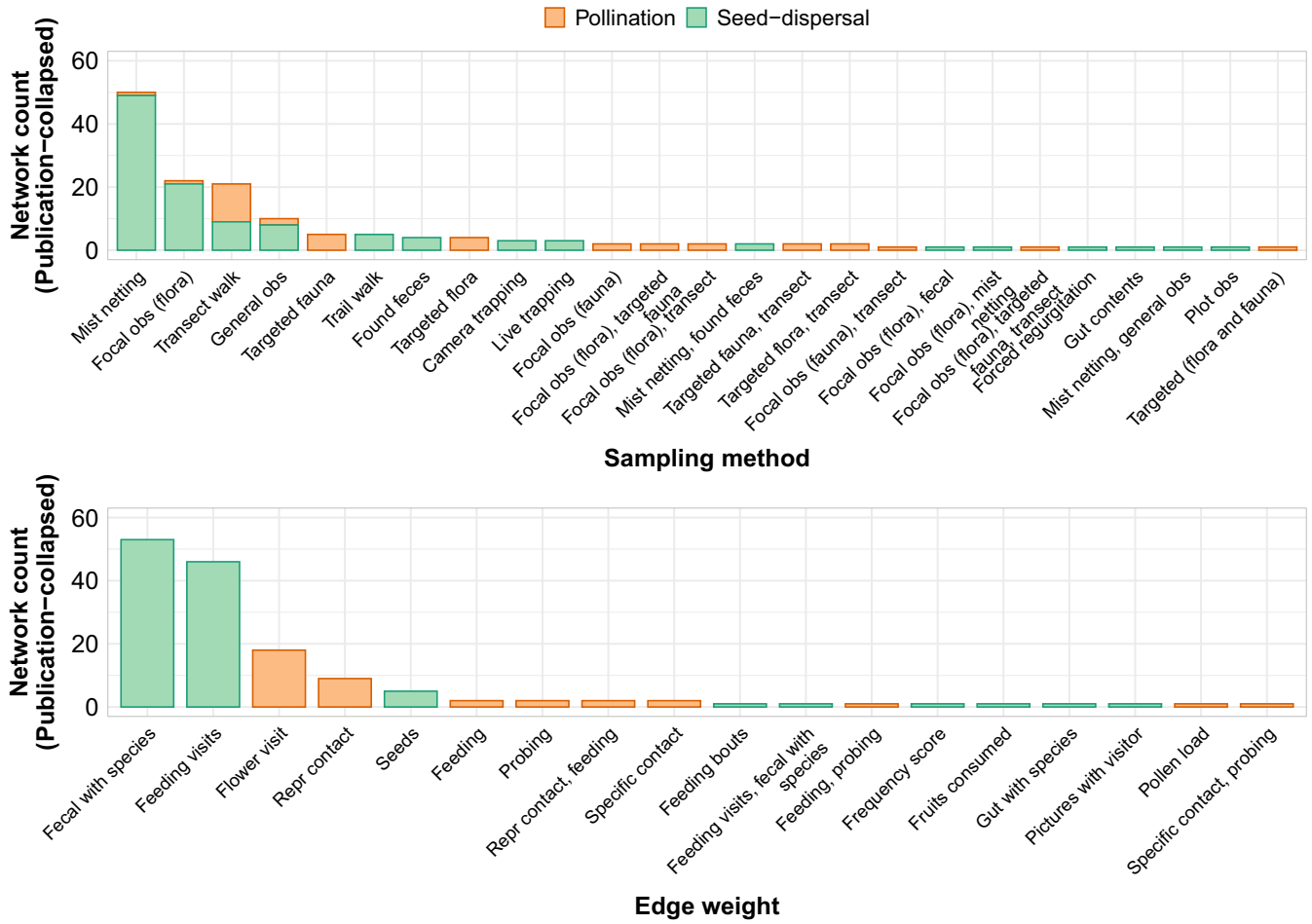

FIGURE 4 Interaction-recording approaches (top panel) and definitions of edge weight units (bottom panel) represented among the 113 pollination and 166 seed-dispersal quantitative networks. Counts were collapsed by publication such that multiple networks from the same publication using the same approach or unit definition were counted once. Pollination networks were sourced from 38 unique publications, compared with 109 for seed-dispersal networks.

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transects and timed observations result in different numbers of unique interactions and degrees of asymmetry in pollination networks. Similarly, Vitorino et al. (2022) found that phytocentric versus zoocentric sampling can yield distinct network topologies, while Souza et al. (2021) documented corresponding important changes in interactions via rewiring and species turnover.

Network construction methodologies

Differences in edge weights

How interaction strength is defined depends on the chosen weighting scheme, and substantial heterogeneity in these units (e.g., visits, fecal samples) across networks limits their comparability. Since these units capture different facets of biological interactions, comparing networks whose edge weights are defined in different units may not be meaningful, while differences in these units can still induce differences in network structure (e.g., Cirtwill et al., 2024; Farine, 2015). For example, in pollination networks, Cirtwill et al. (2024) observed shifts in species roles between visitation- and pollen-based interaction definitions, and Alarcón (2010) found fewer interactions under pollen-load definitions.

Consistent with previous work reporting a similar dichotomy (e.g., Ballantyne et al., 2015; Cirtwill et al., 2024; Dáttilo, 2025), most interaction units in our dataset fell into two categories that differed between pollination and seed-dispersal networks (bottom panel of Figure 4). Treating networks from the same publication as a single entry when they shared a unit definition, pollination networks were mostly defined as flower visits (47%) or reproductive contacts (24%), whereas seed-dispersal networks were mostly fecal samples (48%) or feeding visits (42%). While some units could possibly be merged into broader groups without sacrificing biological meaning (e.g., combining "flower visits" with "probing"), we retain the original categories because edge weight unit definitions vary across networks and are distinguished by the source studies.

Differences in taxonomic node resolution

Variation in node resolution may be unsurprising to most readers. After all, accurate taxonomic identification often requires specialist expertise (Pringle & Hutchinson, 2020; Rodrigues & Boscolo, 2020), meaning that some nodes can only be identified to higher taxonomic levels in practice. Consequently, observed network topology can differ from what would be represented under full species-level identification (Hemprich-Bennett et al., 2021).

More than three-quarters of the open-access networks we analyzed contained at least one node unresolved to species identity (218 of 279 networks), with unresolved nodes comprising an average of approximately 17% of nodes per network (Figure 5). Most partially resolved plant and animal nodes were at the genus level (49%–83%), but the pollinator guild was notably lower at 29%, because many animal nodes had no taxonomic identification whatsoever (e.g., "Unidentified sp.28"; Appendix S1: Table S2). This likely reflects the greater difficulty of taxonomically identifying small insect pollinators than identifying the larger animal species in seed-dispersal networks or the plant species in either network type.

The prevalence of taxonomically unresolved nodes also differed substantially by publication. Whether such nodes are retained in a network can itself depend on deliberate decisions made by the original authors (Pos et al., 2014). At one end of this spectrum, the open-access seed-dispersal networks of Correa et al. (2016) and Peredo et al. (2013) had some of the highest mean proportions of nodes lacking species-level identification (54% and 26%, respectively). By comparison, networks from publications contributing only a single network, which together accounted for roughly half of all networks, generally had lower mean proportions of nodes unresolved to species (20%). Yet, the large SDs of about 19% indicate substantial publication-level variation, since each network in this group represents a different publication.

Biological and environmental factors

Although some broad-scale environmental variables can be consistently assigned across networks when sampling locations are known, many more potentially important topological drivers from the *biological and environmental factors* class are recorded only as qualitative descriptors in the source publication, highlighting distinctive local conditions rather than standardized variables (e.g., Bowker, 2000a). For example, the networks from Kaiser-Bunbury et al. (2010) were sampled to test the effect of eradicating non-native plant species on the Seychelles, with half of the networks from a managed plant-removal site and half from an unmanaged control site. In Partida-Lara et al. (2018), the authors sampled interactions across low-, mid-, and high-altitude sites in three seasons (dry, rainy, and post-rainy) and built separate networks to evaluate how pollinator–flower associations shift along these gradients. In Quitián et al. (2019), multiple separate networks were built from data sampled across fragmented and natural landscapes. Similarly,

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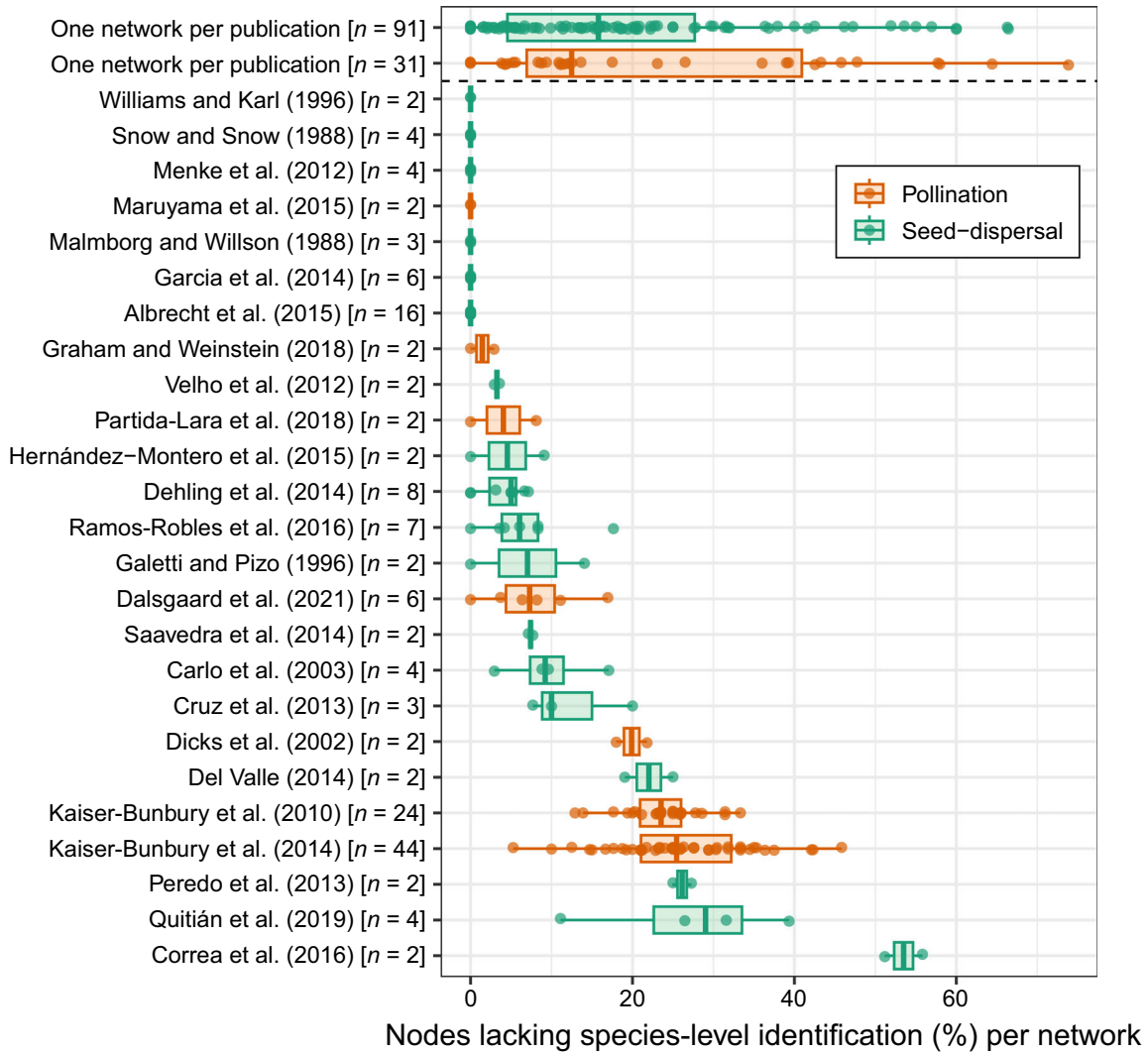

FIGURE 5 Taxonomically unresolved nodes (e.g., "*Anthomyidae* sp.": identified to genus, "Unidentified sp.28": no taxonomic identification) for each of the 113 pollination and 166 seed-dispersal quantitative networks. *n* is the number of networks in each publication grouping.

Albrecht et al. (2015) built multiple networks to reflect communities in old-growth and logged forests, including edge, interior, and fragment locations. Moreover, Dicks et al. (2002) reported two networks, one from an ancient hay meadow and another from a seeded experimental restoration plot. These few examples emphasize how networks are shaped by unique local *biological and environmental factors* that are described idiosyncratically and are difficult to encode in a standardized way for cross-study comparison.

Since these publication-specific *biological and environmental* drivers are rarely recorded as standardized variables, their influence can become attributed to broad-scale environmental predictors that are consistently available across studies. Using latitude as an example—a common explanatory variable (e.g., Dalsgaard et al., 2017; Ollerton & Cranmer, 2002; Pinheiro et al., 2024; Schleuning et al., 2012)—and restricting to publications that contributed multiple networks, linear models yielded several statistically significant associations, with latitude related to the nestedness and modularity of pollination networks and to the nestedness of seed-dispersal networks (Table 2). However, these relationships were not supported once we accounted for the nonindependence of networks from the same publication using linear mixed models with publication as a random effect. This shift does not imply that latitude cannot influence network topology. Instead, it highlights that environmental associations inferred from compiled networks can partly reflect publication-specific clustering.

CORRECTIONS WHEN USING OPEN-ACCESS NETWORKS

Clearly, the drivers of topological variation are expressed differently from one publication to the next. We believe

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TABLE 2 Latitude effects on quantitative network indices estimated using linear models (LMs) and linear mixed models (LMMs) accounting for publication-level nonindependence.

Type	Index	LM β_{lat}	LMM β_{lat}
Pollination	Specialization (H_2')	−0.0008 [−0.0028, 0.0012]	−0.0005 [−0.0038, 0.0028]
	Nestedness (wNODF)	**0.173** [0.059, 0.287]	0.082 [−0.097, 0.261]
	Modularity (DIRTLPAwb+)	**−0.0029** [−0.0045, −0.0013]	−0.0018 [−0.0042, 0.0007]
Seed-dispersal	Specialization (H_2')	0.0008 [−0.0002, 0.0017]	0.0008 [−0.0010, 0.0026]
	Nestedness (wNODF)	**0.140** [0.051, 0.229]	0.144 [−0.047, 0.336]
	Modularity (DIRTLPAwb+)	−0.0003 [−0.0011, 0.0006]	−0.0005 [−0.0022, 0.0013]

Note: LM and LMM were fit to the same subset of data for each network type, restricted to publications contributing multiple networks ($n = 82$ pollination networks from seven publications; $n = 75$ seed-dispersal networks from 18 publications). Within each cell, the first line gives the latitude slope (β_{lat}) and the second line gives the 95% CI in square brackets; bold indicates estimates for which $p < 0.05$. wNODF (Almeida-Neto & Ulrich, 2011) ranges from 0 to 100, while H_2' (Blüthgen et al., 2006) and DIRTLPAwb+ (Beckett, 2016) range from 0 to 1. LMM specification: Index ~ Latitude + (1|Publication).

this arises because collecting network data is difficult and resource-intensive (de Aguiar et al., 2019; Jordano, 2016; Pollock et al., 2025), requiring researchers to develop bespoke (1) *sampling strategies* that reduce effort while still capturing communities in situ and (2) *network construction methodologies* that translate observations into network representations suited to their research questions. Together, these two classes further influence how *biological and environmental factors* are represented in each publication's network topology. Thus, networks from the same publication are more directly comparable than networks sourced from different publications (Brimacombe et al., 2023, 2025), since they typically share *sampling strategies* and *network construction methods* and arise from similar *biological and environmental* contexts.

Although a range of approaches is commonly used in statistical analyses to improve comparability among open-access networks sourced from different publications, their effectiveness in accounting for unwanted topological variation arising from these three classes of drivers remains unclear. Using the 279 bipartite networks, we therefore evaluate several commonly used approaches for addressing some of these sources of variation in cross-study analyses.

Controlling for sampling effort

It is well recognized that network topology is influenced by sampling effort (e.g., Falcão et al., 2016; Fründ et al., 2016; Gibson et al., 2011; Mestre et al., 2022; Nielsen & Bascompte, 2007; Rivera-Hutinel et al., 2012). After all, any network built on very incompletely sampled interactions will likely be topologically different from one more completely sampled.

Controlling for sampling effort, however, is not trivial. Virtually all networks also suffer from varying degrees of incompleteness (Chacoff et al., 2012; Dormann et al., 2017; Fründ et al., 2016). Since concrete estimates of effort are inconsistently reported across publications (e.g., total amount of sampling time), researchers that use open-access networks instead rely on easily evaluated effort proxies derived from the networks themselves. Common proxies include sampling intensity (e.g., Equation 1; Dalsgaard et al., 2017; Luna, Villalobos, Escobar, et al., 2022; Pinilla Cruz et al., 2022; Schleuning et al., 2012, 2014) and network size (e.g., number of species; Brimacombe, Bodner, & Fortin, 2022; Morris et al., 2014). More broadly, attempts to account for sampling effort generally rely on two approaches: (1) observation-based proxies (i.e., total links, edge weights or nodes) and (2) standardization by interaction coverage.

Standardizing by observation-based proxies

When reusing open-access networks, differences in the numbers of nodes and magnitudes of edge weights e_{ij} may reflect differences in sampling effort (Jordano, 2016). Sampling intensity (Equation 1) therefore provides a straightforward, if naive, control that incorporates both. Following Schleuning et al. (2012):

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$$\text{Sampling intensity}(\text{network}_k) = \sqrt{\frac{E}{\text{plants} \times \text{animals}}}, \quad (1)$$

where $E = \sum_i \sum_j e_{ij}$ is the sum of all edge weights, and plants and animals are the numbers of plant and animal nodes, respectively.

Potential issues

Variation in sampling intensity across open-access networks partly reflects differences in the numbers of plant and animal species and cannot be interpreted solely as variation in sampling effort. This is problematic since network size can itself reflect genuine biological variation and other publication-specific drivers of topology.

To show how network size enters the sampling intensity metric, let $\bar{s}$ denote average node strength (i.e., the mean sum of edge weights per node) in a bipartite network. Then

$$2E = \bar{s}(\text{plants} + \text{animals}) \Rightarrow \text{Density} = \frac{E}{\text{plants} \times \text{animals}} = \frac{\bar{s}}{2}\left(\frac{1}{\text{plants}} + \frac{1}{\text{animals}}\right).$$

If plants and animals increase at similar rates and $\bar{s}$ remains approximately constant across networks, then

$$\text{Sampling intensity} \propto N^{-1/2}, \quad (2)$$

where $N = \text{plants} + \text{animals}$. Indeed, after log-linearizing Equation 2, we find that observed sampling intensities across the 279 open-access networks are partially consistent with the predicted $N^{-1/2}$ scaling ($R^2 = 0.20$, Figure 6A). Thus, observed scaling confirms that sampling intensity is not a pure measure of sampling effort but can vary simply due to differences in the number of species represented in the networks.

Sampling intensity also covaries with the very topological indices of interest, further complicating its interpretation (Figure 6B–D). Commonly used quantitative bipartite topological indices, including nestedness (Almeida-Neto & Ulrich, 2011) and modularity (Beckett, 2016), exhibit statistically significant moderate-to-strong linear relationships with log-transformed sampling intensity across the bipartite networks ($R^2 = 0.46$ and 0.24, respectively). While still statistically significant, this association was extremely weak ($R^2 = 0.02$) for the specialization index H'_2 (Blüthgen et al., 2006). Together, these patterns raise two intertwined concerns. First, adjusting for sampling intensity (or network size) risks obscuring or eliminating genuine ecological signals present in network topology when adopting these indices (Luna, Villalobos, & Dáttilo, 2022; Pinheiro et al., 2024). Second, omitting sampling intensity when evaluating topology as a response variable in regression analyses may inflate goodness-of-fit measures (Brimacombe, Bodner, & Fortin, 2022).

Standardizing by interaction coverage

Another approach to standardizing networks by sampling effort is interaction-based rarefaction (Blüthgen & Staab, 2024). Generally, networks with greater total edge weight E are repeatedly subsampled to a common total edge weight, typically defined by the least-sampled network in the set, and network indices are recalculated for each subsample (Blüthgen & Staab, 2024; Morris et al., 2014; Pellissier et al., 2018). Repeating this procedure many times yields an average estimate for each network at an attempted standardized level of sampling.

Potential issues

A potential limitation of interaction-based rarefaction is that standardizing interaction coverage may not remove other publication-specific sources of variation in network topology. To evaluate this, we rarefied each network to 100 interactions 500 times, retaining only networks with at least the target number of interactions at each rarefaction depth (90% of networks). As a sensitivity analysis, we repeated the procedure at depths of 50 and 200 interactions, which retained 98% and 69% of networks, respectively. Publication groupings were recalculated at each rarefaction depth based on the number of eligible networks remaining. We then contrasted dispersion within publications (publications represented by multiple networks) against variation between publications (publications represented by a single network), reasoning that persistent within-publication clustering after rarefaction could indicate that differences in interaction sampling intensity alone cannot explain publication-specific variation in network topology.

Consistent with this concern, rarefaction did not remove the greater topological similarity observed among networks from the same publication. Across specialization, nestedness, and modularity, SDs of rarefied network indices were, on average, 77% larger between publications than within publications (Table 3). This result was confirmed in sensitivity analyses at 50 and 200 interactions, with between-publication SDs averaging 76% and 93% larger than within-publication SDs, respectively (Appendix S1: Tables S4 and S5). Thus, standardizing networks to the same number of interactions was insufficient to remove publication-specific variation in topology.

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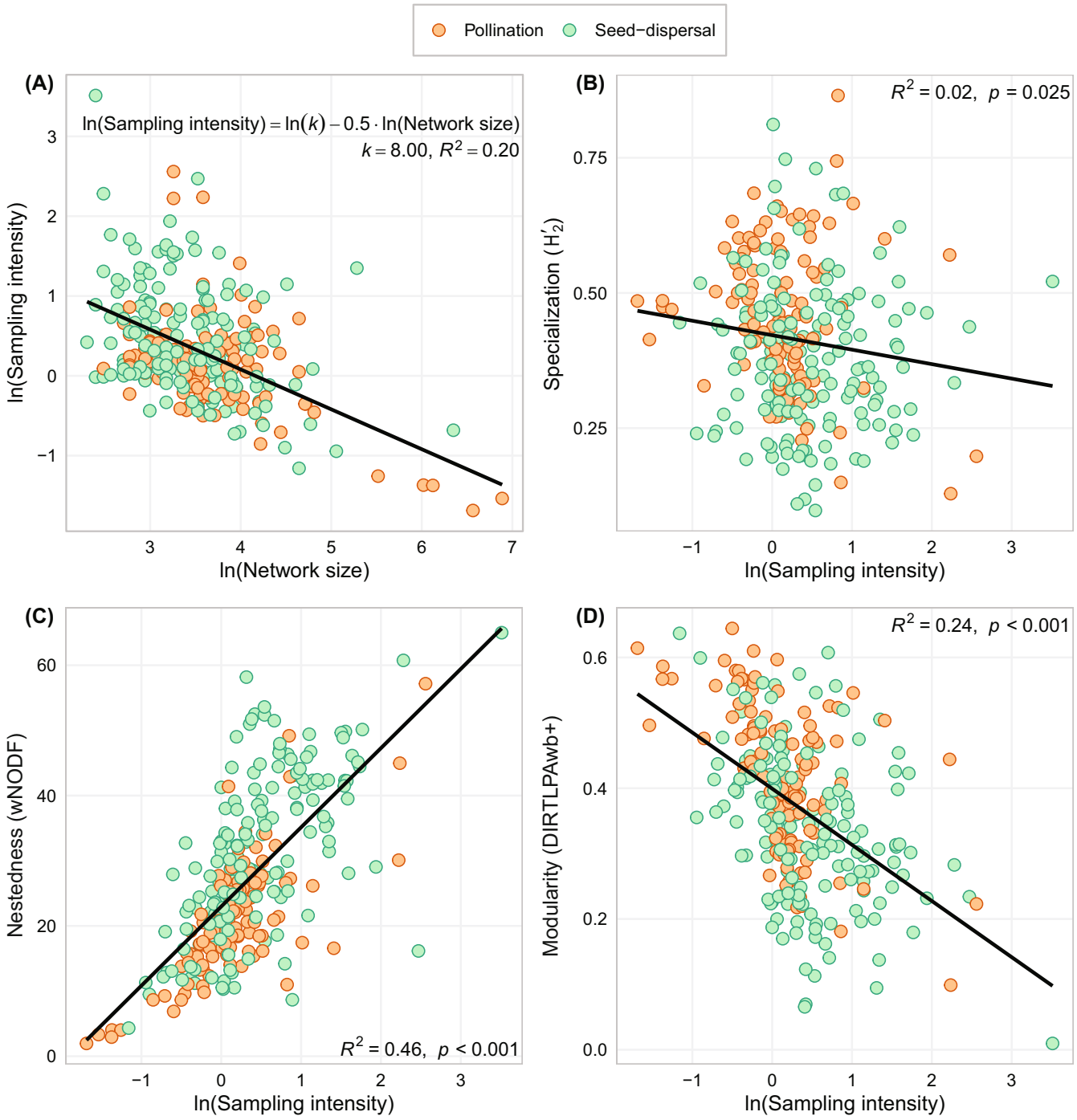

FIGURE 6 Relationships between sampling intensity (Equation 1) and (A) network size (plant + animal), with the expected scaling from Equation 2, and (B–D) three quantitative topological indices, for each of the 113 pollination and 166 seed-dispersal networks.

While some within-publication similarity may reflect shared *biological or environmental* conditions, rarefaction cannot standardize differences in *sampling strategies* beyond sampling intensity or in *network construction methodologies*. This clustering indicates that networks from the same publication remain nonindependent after rarefaction and that publication-specific differences unrelated to the biological relationship of interest may remain embedded in network topology, potentially biasing cross-study inference.

Controlling for publication

Theoretically, if information on the topological drivers were consistently available across open-access networks,

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TABLE 3 SDs of quantitative network indices after rarefaction to 100 interactions per network, comparing networks from publications contributing a single network with those from publications contributing multiple networks.

Type	Indices	SD	
		One network per publication	Multiple networks per publication
Pollination	Specialization (H_2')	0.17	0.10
	Nestedness (wNODF)	9.56	4.19
	Modularity (DIRTLPAwb +)	0.17	0.08
Seed-dispersal	Specialization (H_2')	0.12	0.09
	Nestedness (wNODF)	10.10	7.77
	Modularity (DIRTLPAwb +)	0.13	0.07

Note: Networks were rarefied to 100 interactions 500 times, and index values were averaged across iterations for each network before calculating SDs among networks within publication groups. Of the pollination networks, 74 came from seven "Multiple networks per publication" groups and 31 from the "One network per publication" group; corresponding values for seed-dispersal networks were 64 networks from 16 groups and 81 networks, respectively. "Multiple networks per publication" values were unweighted averages of publication-specific SDs. Publication groupings were recalculated at each rarefaction depth based on the number of eligible networks remaining. See Appendix S1: Table S3 for full results by publication.

their influence could be directly controlled. The absence of such metadata (e.g., Devictor & Bensaude-Vincent, 2016; Kita et al., 2022; Poisot et al., 2016), however, means that these drivers cannot be explicitly accounted for in cross-study syntheses.

A tempting workaround is to instead account for the publication-specific drivers of topology by controlling for the publication source of each open-access network. This has been done in several studies by including publication identity as a random effect (e.g., Brimacombe, Bodner, Michalska-Smith, et al., 2022; García-Callejas et al., 2026; Morris et al., 2014).

Potential issues

One of the main limitations of using publication identity to account for potential non-commensurability among open-access networks is that publication-specific variation in topology cannot always be empirically separated from variation unique to individual networks. When a publication contributes only a single network, there is no within-publication replication with which to distinguish a "publication effect" from properties unique to that network. This can affect a large proportion of open-access networks. In our dataset, 122 of 279 bipartite networks came from a publication that produced only a single network.

This is consequential since publication-specific variation can alter apparent ecological relationships. When we restricted analyses to publications contributing at least two networks—where within-publication replication allows publication-specific clustering to be evaluated—several latitudinal relationships that were statistically significant for explaining topology when networks were treated as independent were no longer supported after publication identity was included as a random intercept (Table 2).

Second, adjusting for publication does not address the core issue since the primary uncertainty is whether networks drawn from different publications are comparable in the first place. Although publication identity can always be included, say as a random effect, it does not explicitly account for differences in, for example, *sampling strategies* or *network construction methodologies*. This means that networks built using fundamentally different approaches can still be analyzed together despite unresolved differences in how they were sampled and constructed, even after publication identity is accounted for.

Network null models

Network null models have become standard tools for addressing sampling differences in open-access bipartite networks perhaps because they, like sampling intensity, rely solely on the network itself. Null models typically reshuffle edge weights while preserving each species' total edge weight to test whether those totals are sufficient to reproduce observed topology (Dormann et al., 2008). In reality, those totals partly reflect the interaction-recording process, and so they are not independent of network topology. Consequently, a null model conditioned on species' total edge weights can only test whether these totals are sufficient to explain a network's topology; it cannot test whether these totals are the cause of this structure (or vice versa), a problem termed the "chicken-or-egg dilemma" by Fort et al. (2016).

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To quantify departures from null expectations, the observed empirical network index T (e.g., nestedness, modularity, specialization) is expressed relative to the mean of its null distribution, $\overline{T}_{\text{null}}$, computed from n null model realizations (n on the order of 10^3) using either a difference or a normalized score:

$$\Delta_{\text{null}} = T - \overline{T}_{\text{null}}, \tag{3}$$

$$z_{\text{null}} = \frac{\Delta_{\text{null}}}{\sigma_{T_{\text{null}}}}, \tag{4}$$

where $\sigma_{T_{\text{null}}}$ is the SD of T across null model realizations. Note: we suppress the dependence of Δ and z on the specific index T for simplicity in this text. Differences (Equation 3) have commonly served as response variables in regression analyses when evaluating network topology across spatial scales (e.g., Brimacombe, Bodner, Michalska-Smith, et al., 2022; Dalsgaard et al., 2017; Maruyama et al., 2024; Schleuning et al., 2014; Simmons et al., 2018; Sonne et al., 2020).

Patefield network null models

The Patefield algorithm (Patefield, 1981) is one of the most prominent ecological null models adopted in the context of bipartite networks (e.g., Correa et al., 2016; Dalsgaard et al., 2017; Dormann et al., 2009; Gama et al., 2025; Mello et al., 2011; Morrison et al., 2020; Partida-Lara et al., 2018; Peredo et al., 2013; Quitián et al., 2019; Simmons et al., 2018; Vázquez & Aizen, 2003).

Operationally, this algorithm preserves each species' total edge weight while redistributing interaction units across the network (Figure 7). It is often regarded as the gold standard for bipartite network null models (Blüthgen & Staab, 2024), as it explores the full arrangement space allowed and samples uniformly across distinguishable arrangements. Uniformity here is with respect to distinguishable allocations of interaction units (i.e., each integer unit of edge weight is treated as distinct). When arrangements are collapsed to indistinguishable configurations, the resulting distribution over configurations is generally nonuniform (see Appendix S1: Section S5 for more information).

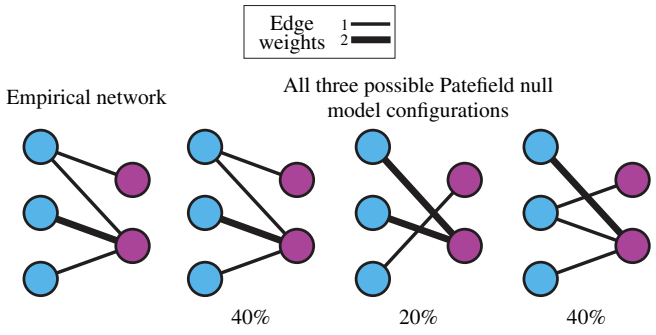

FIGURE 7 Example of the Patefield algorithm for generating quantitative bipartite network null models. Percentages are the probability of each network configuration. The first and last null model configurations are topologically equivalent. Illustration by Chris Brimacombe.

Potential issues

As with rarefaction, a potential limitation of Patefield null correction is that it preserves the marginal totals of each empirical network and therefore cannot remove publication-specific variation encoded in those totals or arising from other topological drivers not addressed by the null model. In other words, the important question is not whether the null model randomizes interaction weights as designed, but whether this randomization is sufficient to remove the publication-specific structure that could bias cross-study comparisons of open-access networks. We therefore tested whether publication-specific clustering persisted after Patefield null correction. Using 1000 Patefield randomizations per empirical network, SDs of Patefield-corrected indices (i.e., $\Delta_{\text{Patefield}} = T - \overline{T}_{\text{Patefield}}$; Equation 3) were, on average, 81% larger between publications than within publications across all indices (nestedness, specialization, and modularity; Table 4). Thus, even after Patefield null correction, networks sourced from the same publication remained more topologically similar than networks sourced from different publications. As discussed above, this residual clustering likely reflects the same publication-specific mixture of *biological and environmental factors*, *sampling strategies*, and *network construction methodologies*, indicating that networks from the same publication remain nonindependent after Patefield null correction and that publication-specific differences may remain embedded in network topology, potentially biasing cross-study inference. The normalized $z_{\text{Patefield}}$ (i.e., $\Delta_{\text{Patefield}}/\sigma_{T_{\text{Patefield}}}$; Equation 4) likewise did not eliminate the publication effect, with SDs on average 221% larger between than within publications across all indices (Appendix S1: Table S7).

Maintaining network connectance: Vázquez network null model

Among the null model algorithms used to shuffle entries in a network, one additional approach is particularly noteworthy. The "Vázquez null model" (`bipartite::`

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TABLE 4 SDs ($\sigma_{\Delta_{\text{Patefield}}}$) of Patefield null-corrected quantitative topological indices (Equation 3), based on 1000 null model replicates per network (Patefield, 1981), comparing networks from publications contributing a single network with those from publications contributing multiple networks.

Type	Indices	SD ($\sigma_{\Delta_{\text{Patefield}}}$)	
		One network per publication	Multiple networks per publication
Pollination	Specialization (H_2')	0.15	0.10
	Nestedness (wNODF)	17.79	5.61
	Modularity (DIRTLPAwb+)	0.10	0.07
Seed-dispersal	Specialization (H_2')	0.14	0.09
	Nestedness (wNODF)	12.17	6.78
	Modularity (DIRTLPAwb+)	0.10	0.07

Note: Of the 113 pollination networks, 82 were from seven "Multiple networks per publication" groups and 31 from the "One network per publication" group; corresponding values for the 166 seed-dispersal networks were 75 networks from 18 groups and 91 networks, respectively. "Multiple networks per publication" values were averages of publication-specific $\sigma_{\Delta_{\text{Patefield}}}$, with each publication contributing equally regardless of the number of networks. See Appendix S1: Table S6 for results by publication.

TABLE 5 SDs ($\sigma_{\Delta_{\text{vaznull}}}$) of Vázquez null-corrected quantitative topological indices (Equation 3), based on 1000 null model replicates per network (Vázquez et al., 2007), comparing networks from publications contributing a single network with those from publications contributing multiple networks.

Type	Indices	SD ($\sigma_{\Delta_{\text{vaznull}}}$)	
		One network per publication	Multiple networks per publication
Pollination	Specialization (H_2')	0.13	0.07
	Nestedness (wNODF)	7.32	5.02
	Modularity (DIRTLPAwb+)	0.10	0.06
Seed-dispersal	Specialization (H_2')	0.11	0.07
	Nestedness (wNODF)	8.82	5.00
	Modularity (DIRTLPAwb+)	0.09	0.06

Note: Of the 113 pollination networks, 82 were from seven "Multiple networks per publication" groups and 31 from the "One network per publication" group; corresponding values for the 166 seed-dispersal networks were 75 networks from 18 groups and 91 networks, respectively. "Multiple networks per publication" values were averages of publication-specific $\sigma_{\Delta_{\texttt{vaznull}}}$, with each publication contributing equally regardless of the number of networks. See Appendix S1: Table S9 for results by publication.

`vaznull`; Vázquez et al., 2007) maintains both edge weight totals (approximately) and the number of 0s (i.e., non-interactions) for each node, aiming to represent the idea that in a network some proportion of links are "forbidden" by incompatible traits (e.g., species not co-occurring in time).

Potential issues

We similarly tested whether publication-specific clustering persisted under the Vázquez null model. Consistent with both rarefaction and Patefield null correction, this approach did not eliminate publication-specific variation in network topology. Using 1000 `vaznull` replicates per empirical network, SDs of Vázquez-corrected indices ($\Delta_{\texttt{vaznull}} = T - \overline{T}_{\texttt{vaznull}}$; Equation 3) were, on average, 64% larger between publications than within publications across all indices (nestedness, specialization, and modularity; Table 5). This contrast was even greater for the normalized $z_{\texttt{vaznull}}$ ($\Delta_{\texttt{vaznull}}/\sigma_{T_{\texttt{vaznull}}}$; Equation 4), for which SDs were on average 165% larger between than within publications (Appendix S1: Table S10).

MAXIMIZING THE UTILITY OF OPEN-ACCESS SPECIES INTERACTION NETWORKS

Despite our critiques of open-access networks, approaching community ecology through a network lens still retains considerable potential. We see two

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broad uses that are especially fruitful. One is advancing our understanding of empirical communities. Unlike some aspects of theoretical ecology—for instance, the complexity-stability debate (Allesina & Tang, 2015; May, 1972), where interactions are assumed to be random—researchers adopting a network perspective generally seek to depict more "real" community topologies that are nonrandom (Landi et al., 2018; Tang et al., 2014). Networks have, for example, been used to assess the stability and resilience of empirical communities (Dunne, 2006; Keyes et al., 2024; Landi et al., 2018), identify keystone species (Jordán et al., 2006; Mello et al., 2015), and analyze species' functional roles via motifs (McLeod et al., 2020; Simmons et al., 2019). A deeper understanding of these communities may, in turn, improve our ability to predict their future responses (Delmas et al., 2019). Naturally, this suggests a second pathway, namely, when data are collected in a standardized manner across sites or through time, a network approach may reveal new ways to monitor or identify areas to protect ecological communities. Perhaps since interactions are often lost before species themselves (Valiente-Banuet et al., 2015), tracking changes in network topology could potentially provide an early warning of anthropogenic stressors that may disrupt communities (e.g., Bartley et al., 2019; Ward et al., 2025). Moreover, networks could potentially extend conservation prioritization beyond species counts by identifying places for conservation action where key interactions or interaction diversity are concentrated (Dansereau et al., 2025; Harvey et al., 2017).

As the saying goes, "If it is worth doing, it is worth doing right." Then how do we do this right? It starts with being clear about *why* an analysis using open-access networks is being undertaken, and then investing the necessary effort to do it well. What "doing it well" looks like may differ slightly depending on whether the goal is to gain insight into the ecology of a community or to inform conservation-related decisions. The next two sections briefly address these two areas.

On primary research of species interaction networks

Overall, our goal is to strengthen, rather than to dissuade, the scientific use of open-access species interaction networks for learning more about community structure. Like others (e.g., Cohen et al., 1993; Ollerton & Cranmer, 2002; Pellissier et al., 2018; Winemiller, 1990), we argue that if large numbers of communities are to be investigated as networks to begin to determine general ecological rules, open-access data collection must be conducted with sufficient intentionality to support meaningful synthesis and comparison. This means that networks should be deliberately built using consistent *sampling strategies* and *network construction methodologies* to investigate the *biological and environmental factors* that structure communities across large spatiotemporal extents.

Achieving commensurable networks reflecting communities across the globe would require difficult, high-level decisions. While we do not attempt to prescribe specific decisions regarding *sampling strategies*, *network construction methodologies*, or *biological and environmental factors*—as that would be deciding which scientific questions should be most of interest—several are unavoidable. These include which types of communities to prioritize (e.g., pollination, seed dispersal, food webs), how to characterize the fitness consequences of species interactions (e.g., Dáttilo, 2025; Dormann, 2023; Ollerton et al., 2025), and how to document the local biological and environmental conditions of sampled communities (e.g., Bowker, 2000b). Decisions such as these often involve genuine trade-offs rather than a single optimal choice. For example, retaining unresolved taxa in networks preserves observed interactions that would otherwise be discarded but introduces heterogeneity in taxonomic resolution, whereas removing them improves taxonomic consistency at the cost of losing observed interactions and potentially introducing bias if taxonomic resolution is nonrandom. Our recommendations therefore focus on the consistency and transparency of these decisions so that researchers reusing open-access networks can assess whether differences among studies limit their commensurability. Altogether, such an effort would be substantial, costly, and likely infeasible for any single research lab. However, large-scale standardized field campaigns do indeed exist, such as the National Ecological Observatory Network in the United States (Keller et al., 2008).

Even under a large-scale collaboration, however, these networks will primarily support exploration of broad patterns and will rarely be sufficient for assessing community-specific hypotheses. For instance, claims that keystone species can be identified by their centrality in a network require keystone status first be defined independently of the network, for example, by using evidence of functional impact, and then evaluated against interaction data. Alternatively, network centrality can be used to nominate candidate keystone species, but their functional roles must still be validated independently. In either case, sampling must prioritize the species that contribute most to the ecosystem function under consideration (e.g., carbon sequestration), as omitting these dominant species undermines the validity of any conclusions. As general-purpose

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networks are not built around a single functional question, we suggest that their greatest value lies in capturing overall community structure rather than resolving specific mechanistic hypotheses.

On conservation-oriented applications of species interaction networks

Species interaction networks are often celebrated as potential guides for decision-makers on the development and evaluation of habitat design, restoration planning, species reintroduction, and conservation targets (Dansereau et al., 2025; Fortin et al., 2021; Harvey et al., 2017; Windsor et al., 2023). The availability of open-access networks supports these endeavors; however, the ease with which the classic bipartite networks and food web diagrams can be interpreted often obscures the field realities that shape them (Dansereau et al., 2025).

For this reason, we argue that open-access networks need to be cautiously used to inform conservation and grounded in in situ sampling at the locations of interest. Their utility depends on, among other things, clearly knowing what they represent, including the taxa targeted during sampling, the meaning of interaction weights, and whether recorded interactions reflect mutualistic outcomes or other behaviors (e.g., nectar robbing; Aubert et al., 2026) that may not support management goals. Where this information is unclear or incomplete, local sampling can establish which species and interactions occur at the location of interest and reveal where an open-access network provides only a partial representation of the community. General patterns described using open-access interaction networks, such as reduced stability under fragmentation (Grass et al., 2018) or shifts in modularity with global change (Dalsgaard et al., 2013), can provide high-level guidance, but rarely provide the fine-resolution information needed by practitioners for site-specific decisions. Thus, conservation applications typically demand case-specific scrutiny grounded in rigorous, and preferably long-term, locally collected data (Lussier et al., 2025).

Metawebs illustrate particularly well both the utility and limitations of compiled interaction data for conservation. A metaweb compiles interactions that have been documented across multiple studies or locations (e.g., in open-access networks) and can then be filtered to the species present at a particular location to construct a potential local interaction network (Gravel et al., 2019). This provides a way to build such a network for the location of interest without having to directly document every interaction there. However, metawebs inherit the *sampling strategies* and *network construction methodologies* that are specific to their source studies, meaning that the apparent presence or absence of interactions may partly reflect how and where those studies were conducted (Brimacombe et al., 2024; Dansereau et al., 2025). Consequently, predictions derived from these compilations are best treated as hypotheses to be evaluated and refined through local sampling (e.g., Banville et al., 2025), with those observations subsequently incorporated to improve the representation of interactions at the location of interest.

CONCLUSION

Open-access quantitative bipartite networks are widely reused in comparative analyses. However, our review of the original publications that produced these networks, together with what is evident from the node identities in the networks themselves, reveals substantial heterogeneity in how ecological communities were sampled, the biological and environmental contexts they experienced, and how those observations were translated into networks. This is consequential since open-access networks are commonly used to evaluate the influence of biological and environmental drivers on network topology, making it necessary to distinguish differences arising from sampling and network construction from the ecological relationships of interest. Yet doing so remains difficult. Many commonly used methods intended to improve comparability are derived from the network itself and are therefore not independent of the topological properties whose comparison they are intended to facilitate. In our analyses, such methods either failed to remove topological variation associated with the source publication or covaried with the very network properties of interest. Adjustment for publication identity provides an external means of accounting for some of this heterogeneity and, importantly, altered several estimated relationships. But publication identity is only a proxy for the many differences in sampling, network construction, and biological context among studies, and its inclusion does not establish that the networks are otherwise commensurable. More directly addressing this limitation would require additional metadata on sampling, network construction, and biological context, which are often incomplete or unavailable. Altogether, we contend that networks pooled from many publications may provide an uncertain basis for cross-study comparative inference from topology, particularly when the goal is to infer general drivers or rules of network structure.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

Data and code (Chrisb590 and Cazelles, 2026) are available in Zenodo at https://doi.org/10.5281/zenodo.23265608.

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